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***Candidatus* Liberibacter americanus induces significant reprogramming of the transcriptome of the susceptible citrus genotype**

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In Brazil, *Huanglongbing* (HLB) is caused by *Candidatus* *Liberibacter americanus* (CaLam) and *Ca. L. asiaticus* (CaLas). Both species are vectored by the Asian citrus psyllid and are restricted to the phloem of infected citrus, where they promote a severe imbalance in the translocation of nutrients and other important substances along the plant. Several studies of the transcriptional response of citrus to HLB have been reported, but only for infection caused by CaLas. This study evaluated the transcriptional reprogramming of a susceptible genotype (Pera sweet orange) challenged with CaLam, using a customized 385K microarray chip. The analyses showed that a large number of genes and biological processes were significantly altered upon CaLam infection. Among the changes we highlight induction of zinc transporters, modulation of enzymes related to sugar metabolism, decreased photosynthesis, induction of several defense-related genes and modulation of enzymes regulating ROS production. Several biological processes reported as differentially modulated upon infection with CaLas responded similarly to CaLam. The large number of receptor-like proteins, PR genes, NBS-LRR and transcription factors (such as WRKY and MYB) found showed that even a susceptible citrus genotype is able to actively respond to infection by CaLam, as reported for CaLas. Twenty candidate genes were selected for validation in symptomatic and asymptomatic PCR-positive leaves of Hamlin sweet orange infected with CaLas or CaLam. Finally, using *in silico* approaches, we compared our results with all published studies using CaLas to hypothesize a global feature of the defense/susceptibility mechanisms of citrus in response to the bacteria. These results have been explored in selection of target genes for genetic engineering to control HLB. Also, further transcriptome (RNAseq) experiments using tolerant and susceptible citrus genotypes infected with CaLam or CaLas using different time points are in progress to investigate the dynamics of expression of these genes during early stages of infection.

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